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Dynamin-1-like protein inhibition drives megamitochondria formation as an adaptive response in alcohol-induced hepatotoxicity

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Abstract

Despite the growing global burden of alcoholic liver diseases, therapeutic options are limited and novel targets are urgently needed. Accumulating evidence suggests that mitochondria adapt in response to ethanol and formation of megamitochondria in the livers of patients is recognized as a hallmark of alcoholic liver diseases. The processes involved in ethanol-induced hepatic mitochondrial changes, the impact on mitochondria-shaping proteins, and the significance of megamitochondria formation remain unknown. In this study, we investigated the mitochondrial and cellular response to alcohol in hepatoma cell line VL-17A. The mitochondrial architecture rapidly changed after 3 or 14 days of ethanol exposure with double-pronged presentation of hyper-fragmentation and megamitochondria and cell growth was inhibited. Dynamin-1-like protein (Drp1) was identified as the main mediator driving these mitochondrial alterations and its genetic inactivation was determined to foster megamitochondria development, preserving the capacity of the cells to grow despite alcohol toxicity. The role of Drp1 in mediating megamitochondria formation in mice with liver-specific inactivation of Drp1 was further confirmed. Finally, when these mice were fed with ethanol, the presentation of hepatic megamitochondria was exacerbated compared to wild type fed with the same diet. Ethanol-induced toxicity was also reduced. Our study demonstrates that megamitochondria formation is mediated by Drp1 and this phenomenon is a beneficial adaptive response during alcohol-induced hepatotoxicity.

Introduction

Alcoholic liver diseases (ALD) encompass a number of clinical presentations ranging from simple steatosis to steatohepatitis, fibrosis, and cirrhosis and can also manifest as severe alcoholic hepatitis. The pathobiology of ALD is not fully elucidated and this has led to a lack of treatment options for this disorder which represents one of the 10 most common causes of death in the Western World¹.

Mitochondria play an essential role within the complex disease processes associated with ALD not only as the central location for alcohol metabolizing enzymes, but also as active mediators in the response to alcohol toxicity^{2, 3}. In hepatocytes, ethanol oxidation perturbs the homeostasis of several mitochondrial pathways involved in glucose/lipid metabolism and energy conversion. Ethanol also dramatically increases oxidative stress, which directly drives changes in mitochondrial proteins, lipids, and mitochondrial DNA affecting functionality and cellular viability⁴. Importantly, the morphology and the functionality of mitochondria are strictly correlated and mitochondrial dynamics, with cycles of fusion (binding of two organelles) and fission (mitochondrial fragmentation) constantly adjusting mitochondrial shape to maintain a pool of fully operative organelles. The balance between mitochondrial fusion and fission determines the architecture of the mitochondrion which is necessary for the preservation of cellular and tissue integrity. These processes regulate the selective removal of damaged organelles (mitophagy) through fission and the maintenance of the bioenergetic efficiency through fusion⁵. Fusion and fission are driven primarily through the activity of multiple “mitochondria-shaping proteins” (MSP) which act together to maintain a balance between these two antagonistic events⁶. When either process is blocked, the final morphology of the mitochondrion is the consequence of unopposed progression towards the other side of the equilibrium. Although new members of this family are continuing to be discovered, the best characterized include Mitofusin-1 and -2 (Mfn1, Mfn2), which localize on the outer mitochondrial membrane and are essential for mitochondrial tethering to initiate the fusion process⁷. Conversely, dynamin-1-like protein (Drp1, gene: *DNM1L*) drives

fragmentation; this cytosolic GTPase protein when activated translocates to mitochondria and assembles in multimers to constrict and fragment the organelle⁸⁻¹⁰. Several proteins localized on the outer mitochondrial membrane have been proposed as Drp1 receptors, including mitochondrial fission 1 protein (Fis1), mitochondrial fission factor (Mff), and mitochondrial dynamics protein MID49 and mitochondrial dynamics protein MID51¹¹; however, their exact mechanisms of action and the effect on mitochondrial morphology are still under debate¹². Alterations in MSP or in the equilibrium between fusion and fission have been associated with the pathogenesis of several neurodegenerative and metabolic disorders^{13, 14}.

The current study elucidates the impact of ethanol on mitochondrial morphology in the liver and identifies for the first time the main regulator involved in the morphological changes induced by ethanol on hepatic mitochondria, opening new perspectives for potential therapeutic strategies in ALD.

Materials and methods

Cellular models

Human hepatoma VL-17A cell line, stably expressing alcohol dehydrogenase (ADH) and CYP2E1¹⁵, were cultured in complete DMEM containing zeocin and geneticin at 400µg/mL in the presence/absence of ethanol (EtOH) at 100mM for 3 (D3) or 14 days (D14) and EtOH replaced at every passage. Treated cells were kept in an incubator saturated with EtOH to minimize evaporation (opened petri dish containing 200mM ethanol).

Three cell models were derived from VL-17A. VL-17A cells transiently transfected with mitochondrially targeted RFP to label mitochondria (mtRFP; Clontech, Saint-Germain-en-Laye, France) according to manufacturer's guidelines (Neon transfection system, Life technologies, Paisley, UK). VL-17A cells transiently transfected with a plasmid expressing mtRFP and a Drp1 mutant (Lys 38 to Ala) that acts as dominant negative (Drp1-K38A) and

disables the fragmentation activity of Drp1^{9, 10} (pcDNA3-Drp1-K38A was a kind gift of Professor Luca Scorrano, University of Padova, Italy). VL-17A cells stably expressing Drp1-K38A and/or enhanced green fluorescent protein (eGFP) generated through lentiviral transduction.

Animal model

Drp1 (Dnm1l) Flox/Flox mice (C57BL/6/129) were generated as described previously¹⁶ and crossed with Albumin-Cre mice (Alb-Cre, C57BL/6) (Jackson Laboratory, Bar Harbor, ME) to obtain mice with liver-specific inactivation of *Drp1 (Dnm1l)* (Alb-Cre+Drp1) and compared to wild type (WT, Alb-Cre-Drp1) male C57BL/6 J mice (Jackson Laboratories). Alb-Cre-Drp1 and Alb-Cre+Drp1 mice were divided into two groups and fed either with control diet or with the ethanol diet NIAAA model (10-d *ad libitum* oral feeding with the Lieber-DeCarli ethanol liquid diet (5%v/v) plus a single binge ethanol feeding via gavage (5g/kg)) as previously described¹⁷. All animals received human care. All procedures were approved by the Institutional Animal Care and Use Committee of the University of Kansas Medical Center. Alanine aminotransferase (ALT) levels were measured in the blood of mice using a commercial kit (Liquid ALT Reagents, Pointe Scientific, Canton, MI).

Plasmids, lentiviral preparation, and infection

The bicistronic lentiviral vector pULTRA expressing eGFP was a gift from Malcolm Moore, Memorial Sloan-Kettering Center, New York, NY (Addgene plasmid # 24129)¹⁸ and pULTRA-eGFP-Drp1-K38A was obtained from cloning the Drp1-K38A DNA fragment isolated from pcDNA3-Drp1-K38A between BamHI and EcoRI restriction sites of pULTRA-eGFP and confirmed by nucleotide sequencing. Lentiviral preparations were obtained, as previously described¹⁹. Supernatants were harvested, concentrated, and lentiviral titer measured with QuickTiter™ Lentivirus Titer Kit (Cambridge Bioscience, Cambridge, UK),

then used to infect VL-17A cell line in the presence of 8 µg/mL polybrene (Sigma, Gillingham, UK).

Confocal microscopy

Mitochondria were visualized in VL-17A cells using immunostaining as previously described⁷ after staining with anti-Tom20 (BD Bioscience, Oxford, UK) and NorthernLights anti-mouse IgG-NL557 (R&D Systems, Minneapolis, MN) or in VL-17A cells expressing mtRFP with/without transient expression of Drp1-K38A. Confocal images were collected using the PerkinElmer spinning-disk confocal microscope UltraVIEW (Perkin Elmer, Coventry, UK).

Morphological analysis

- 1) Approximately 50 images (300 VL-17A cells) per condition were collected by confocal microscopy and cells were ranked according to their mitochondrial phenotype and blindly scored using previously reported guidelines^{7, 10}. The three cellular phenotypes (Fig.1A) included: i) hyper-fragmented: cells presenting >50% of mitochondria as small and spherical entities (diameter<1µm); ii) mixed network: cellular presentation of interconnected mitochondrial network with <50% fragmented organelles and elongated mitochondria (length>2µm/width<1µm) concurrently; and iii) hyper-fused (mega): over-interconnected mitochondrial structure with abnormal enlargements including discrete oversized megamitochondria with width and length>1µm according to previously reported categorization recommendations²⁰.

Cell growth and viability assays

Cell growth was assessed at every passage by evaluating the number of viable cells (propidium iodide(-), PI) with growth rate calculated as fold increase per day. Cell proliferation was evaluated using the CellTrace™ Far Red Cell Proliferation Kit (Thermo Fisher Scientific, Basingstoke, UK), according to the manufacturer's guidelines. Early apoptotic or necrotic events were detected by flow cytometric analysis, with V450 Annexin V

(BD Horizon; mark of apoptosis) in addition to PI (Sigma) or 7-aminoactinomycin D (7-AAD) (Biolegend, London, UK) staining. Data were acquired and analyzed on a FACS Canto II flow cytometer using FACS Diva 6.1 software (BD).

Mitochondrial isolation

VL-17A cells were homogenized in isolation buffer (250mM sucrose, 10mM TRIS, 1mM EGTA, pH 7.4) using the Precellys[®]24 grinder (Bertin Technologies, Montigny le Bretonneux, France) with ceramic bead-vials. Mitochondria were then isolated by standard differential centrifugations as previously described²¹. Mitochondrial protein concentration was quantified by Pierce BCA Protein Assay Kit (Thermo Fisher Scientific).

Western Blot Analysis

Protein extracts were obtained from total cell lysate, mitochondrial fraction, and mouse liver homogenate and separated by 12% SDS-PAGE, transferred onto nitrocellulose membranes (GE Healthcare Bio-Sciences AB, Uppsala, Sweden) and analyzed as previously described⁷. The following antibodies (dilution 1:1000) were used: anti-Drp1, anti-Tom20 (BD Bioscience); anti-MiD51 (SMCR7L/MID51) (ProteinTech Europe, Manchester, UK); anti-Mff (Sigma); anti-Mitofusin-1, anti-Mitofusin-2, antipyruvate dehydrogenase kinase 1 (anti-PDK1), anti-actinin (Santa Cruz biotechnology, Heidelberg, Germany); anti- β -actin, anti-VDAC1/Porin (Abcam, Cambridge, UK).

Mitochondrial mass

The mitochondrial mass was quantified by flow cytometry after staining the living cells with 20nM MitoTracker Green FM (Life Technologies) for 30 minutes at 37 °C according to the manufacturer's protocol, in presence of 2 μ g/mL Cyclosporin H (Santa Cruz Biotechnology). Data were acquired and analyzed on a FACS Canto II flow cytometer using FACS Diva 6.1 software (BD).

Mitochondrial respiration

Seahorse XF24 Analyzer (Seahorse Bioscience, Copenhagen, Denmark) was used to measure the mitochondrial oxygen consumption rate (OCR) in untreated/treated VL-17A cells *in situ*. Changes in OCR (nmoles/min) in response to oligomycin (oligo, 1 µg/mL; Sigma), carbonyl cyanide 4-(trifluoromethoxy) phenylhydrazone (FCCP, 0.6 µM; Sigma), and antimycin A (anti, 2 µM; Sigma) were measured and used to calculate the spare respiratory capacity (OCR_{FCCP}/OCR_{basal}) and the coupling efficiency ($1-OCR_{oligo}/OCR_{basal}$). Measurements were repeated in triplicate in three separate experiments and the OCR values normalized for the total protein content, quantified by Pierce BCA Protein Assay Kit (Thermo Fisher Scientific).

Electron Microscopy

Cells or murine liver tissue were fixed with 2% paraformaldehyde and 1.5% glutaraldehyde in 0.1M cacodylate buffer or 2.5% glutaraldehyde in 0.1M phosphate buffer (pH 7.4), followed by 1% OSO_4 . After dehydration, ultrathin sections were stained with uranyl acetate and lead citrate and viewed in a JEM 1011CX or 1010 transition electron microscope (JEOL) as described previously²². The size of megamitochondria was evaluated in the cells using ImageJ 1.49c: images were analyzed in blind and the length and the width of megamitochondria (>1 µm) were measured using the straight line function across each organelle, followed by analyse measure.

Statistical analysis

Continuous variables were expressed as mean ± standard error of the mean (SEM) and categorical variables were described as means of counts and percentages. Comparisons were performed using independent or paired Student *t* test or non-parametric Friedman's analysis of variance for repeated measures, when multiple treatment groups were analyzed simultaneously. Categorical variables (morphological analysis) were analyzed by Chi-square test. Statistics were calculated using MS Excel 2010 (Microsoft, Redmond, WA) and GraphPad Prism 6.07 (GraphPad, La Jolla, CA). Statistical significance was set at $P < 0.05$.

Results

Ethanol exposure severely impairs cellular proliferation and mitochondrial morphology in VL-17A cells, with no impact on mitochondrial mass or functionality

A significant impact on proliferative potential was observed in response to both short and long exposure of ethanol in VL-17A cells (Fig.2A, B). After the short insult the apoptotic and necrotic levels were not significantly different from the controls (Fig.2C), whereas longer alcohol exposure induced a slight but significant increase in the percentage of apoptotic cells (Fig.2C). The measurement of basal mitochondrial respiration rate (Fig.2D) and the calculation of the coupling efficiency as well as of the spare respiratory capacity were not different between the short and long-ethanol cultures compared to the controls (Fig.2E). The mitochondrial mass was also not affected by ethanol exposure (Fig.2F), but remarkable mitochondrial remodelling was observed by confocal and electron microscopy. The untreated cells presented a prevalence of interconnected mitochondrial network, with a balance between fusion/fission, whereas the ethanol-treated cells displayed a significantly different distribution among the three mitochondrial phenotypes both in day3 and day14 cultures (Fig.1A) with more than 14% of the cells exposed to ethanol showing a hyper-fragmented network. With extended exposure to ethanol the presence of oversized and misshapen megamitochondria (Fig.1B) were observed. These abnormalities were also detected by confocal microscopy (Fig.1A), where almost 30% of the cells exposed to day14 ethanol were classified in the hyper-fused/ megamitochondria phenotype.

Extended ethanol exposure affects mitochondrial shaping protein expression in VL-17A cells

Short ethanol exposure in VL-17A cells did not impact the fusion or fragmentation pathways (Fig.3), but prolonged ethanol treatment significantly reduced the mitochondrial translocation of Drp1, the main protagonist driving mitochondrial fragmentation, this was paralleled with an

observed increase in the Drp1 receptor Mff (Fig.3A). Ethanol did not affect the fusion machinery; no changes were observed in Mfn-1 or Mfn-2 (Fig.3B). In WT mice fed with ethanol no significant changes in Drp1 hepatic expression were detected when compared to control animals (Fig.3C).

Drp1 inactivation promotes megamitochondria formation and abrogates ethanol-induced cell growth retardation in hepatoma cells

The analysis of the mitochondrial phenotypes (hyper-fragmented, mixed, and hyper-fused) and the evaluation of ethanol toxicity were performed in the cellular model where the fragmentation pathway was disabled (Drp1-K38A) in comparison to the control VL-17A with active Drp1. In the absence of ethanol, inactivation of Drp1 led to a notable increase in the appearance of hyper-fused megamitochondria (Fig.4 A). Ethanol induced fragmentation in the control VL-17A cells (Fig.4B) but this was completely abolished in the Drp1-K38A cells, which presented an additional increase in megamitochondria formation (Fig.4A). Further to this, the impact of ethanol on cellular growth was evaluated in the stable lines of VL-17A expressing both eGFP and Drp1-K38A (GFP⁺ Drp1-inactive) and the control cells expressing only eGFP (WT Drp1-active). In cultures with Drp1 active growth retardation was observed during ethanol exposure (Fig. 4C). However, inactivation of Drp1, with megamitochondria formation, rescued this growth blockade with percentage of GFP⁺/Drp1-K38A cells significantly increasing over time despite alcohol insult. Moreover, these cells showed a proliferative advantage compared to the GFP⁻ cells in the same culture (Fig.4C).

Drp1 inactivation causes megamitochondria development in murine livers

The hepatic mitochondrial evaluation by electron microscopy in the mice after liver inactivation of Drp1 showed the formation of very enlarged and round shaped organelles

(Fig.5A, B) with the same morphological characteristics of megamitochondria observed in the cellular model after ethanol exposure (Fig.1) as well as previously reported in animal models fed with alcohol²³ or liver biopsies from alcoholic patients²⁴. The incidence of megamitochondria was significantly increased in the liver of these mice after inactivation of Drp1 (Alb-Cre⁺Drp1) compared to the WT (Alb-Cre⁻Drp1) (Fig.5C).

Ethanol exposure causes megamitochondria formation in murine livers and Drp1 inactivation exacerbates this phenomenon and reduces ethanol-induced hepatotoxicity

In both WT mice (Alb-Cre⁻Drp1) and mice with inactive hepatic Drp1 (Alb-Cre⁺Drp1) the ethanol diet induced a significant increase in the percentage of megamitochondria (Fig.5A, B, C), and this effect was significantly more pronounced in mice with inactive Drp1 when compared to WT (Fig.5C). The effect of ethanol on ALT levels was also analyzed and these values were found to be significantly increased in WT mice, but not in mice with inactive Drp1 as shown from the ratios of ethanol vs control diet (Fig.5D).

Discussion

One of the main findings of this study was the profound impact of ethanol on hepatic mitochondrial morphology, including both organelle fragmentation and enlargement. Both short and long exposure of ethanol induced an increase in the hyper-fragmented mitochondrial fraction confirming ethanol-related augmented fission which has previously only been reported in other cell types including human retinal pigment epithelial cells^{25, 26} and alveolar macrophages²⁷. In the hepatoma cell model, ethanol exposure caused an immediate change in mitochondrial shape with significant imbalance of the fusion/fission equilibrium, which was confirmed by the changes in MSP expression observed. These

results suggest that mitochondrial dynamics play an essential role in alcohol-related liver disease and support other studies which have observed hepatic mitochondrial remodelling during alcoholic insults^{28, 29}. In addition, after the prolonged exposure, hyper-fragmentation was accompanied by the formation of disproportionately enlarged megamitochondria. These architectural alterations in hepatic mitochondria were similar to the presentation of enlarged and hyper-fused organelles previously identified in patients and animal models, as one of the consequences of chronic ethanol consumption. Indeed, the detection of megamitochondria in liver biopsies has been regarded as a specific hallmark for alcohol-related liver disease since the 1970s^{23, 30, 31}. In this study extended ethanol exposure induced the formation of megamitochondria in the VL-17A cells, endorsing for the first time the validity of this cell line in studying the phenomenon.

These data suggest that the appearance of megamitochondria after a prolonged/chronic stimulus alongside mitochondrial hyper-fragmentation, is an adaptive mechanism possibly to counteract excessive fission and mitophagy, which unregulated would be highly detrimental to cellular survival^{32, 33}. This seems to represent a response of the hepatocytes to preserve cellular function in the face of a toxic insult with mitochondrial fragmentation facilitating the clearance of dysfunctional organelles via mitophagy. This is supported by reports demonstrating that alcohol stimulates the initiation of autophagy^{34, 35} and that damaged mitochondria and accumulated lipid droplets are the selective target of autophagy induced by acute ethanol exposure³⁶.

In addition, this study identified for the first time the master fission mediator Drp1 as the key player involved in the alcohol-related morphological changes. In our cellular model, the expression of mutated dominant-negative Drp1 (Drp1-K38A) was sufficient to abolish the ethanol-induced mitochondrial hyper-fragmentation and one of the most striking results was the beneficial effect on cell proliferation of Drp1 inhibition in response to ethanol insult. In control cells with active Drp1, ethanol was able to induce a significant growth retardation even after three days of exposure. Indeed, ALD is known to be associated with a significant

loss of hepatocyte proliferation and impaired regeneration, further driving the inability of the liver to deal with the toxic insult due to a reduced capacity to replace dying hepatocytes. This is an area of much interest and many clinical trials are trying to find ways to promote hepatocyte proliferation³⁷. Drp1 inactivation in the VL-17A cells showed a protective effect with the rescue of cell growth retardation induced by ethanol both at 3 and 14 days of toxic exposure. The toxic effect in terms of cell death was probably too mild to be appreciated in this model (data not shown). More importantly, Drp1 inactivation showed a beneficial effect also in the mouse model where the ethanol exposure did not induce significant changes in the release of alanine aminotransferase. This finding is particularly relevant considering the significant and escalating clinical burden of alcohol-related liver disease and therefore the urgent need to develop specific and targeted drugs. Currently, the cornerstone of therapy remains abstinence with supportive treatments and few other options with limited efficacy³⁸. There are no therapies aimed at stopping ongoing ethanol toxicity in hepatocytes, to halt injury and allow time for regeneration and repair. This study gives the initial experimental evidence that targeting mitochondrial dynamics could reduce liver injury by improving the adaptation of hepatocytes to alcohol toxicity. Moreover, it has been recently demonstrated that Drp1 inhibition has a beneficial and protective effect in several other models of liver injury, including hepatotoxicity induced by toxic agents (senecionine³⁹ and cadmium⁴⁰), in animal models of diet-induced steatosis⁴¹ and cholestatic liver injury⁴².

The most important finding of this study is that Drp1 inhibition is able to cause a rapid and extensive formation of megamitochondria, which was confirmed in mouse models with liver-specific inactivation of Drp1. The molecular mechanisms regulating the development of these morphological abnormalities and their influence on cellular responses have not been elucidated to date, but several clinical studies have endorsed the presence of intrahepatic megamitochondria in ALD as beneficial clinical indicators⁴³⁻⁴⁶. Moreover, a recent study has reported that the treatment with Drp1 inhibitor Mdivi-1 in *Triticum aestivum* caused fission retardation with consequent induction of megamitochondria and this has been recognized as

a strategic adaptation of plants to stress⁴⁷. The prospect for the use of Drp1 inhibitors *in vivo* has also become more promising after the demonstration of their prophylactic and therapeutic effects in several models of tissue injury, induced by toxic insult or ischemia/reperfusion damage⁴⁸⁻⁵³. The beneficial advantage of these agents in alcohol-induced liver injury may also be two-pronged due to a decrease of oxidative stress, as associated with Drp1 inhibitors treatment in a murine cardiac arrest model⁵⁴, which plays a fundamental role in alcohol-related hepatotoxicity.

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E.P. designed the study, collected and analyzed the data, and wrote the manuscript. X.M., A.R., A.D., and S.W. performed the experiments and collected the data. V.I. performed experiments and analyzed the data. H.N. and H.S. generated the mouse model. R.W. designed the study and wrote the manuscript. W.D. collected and analyzed the data. S.C. designed the study, analyzed the data, and wrote the manuscript.

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Figure Legends

Figure 1. Ethanol (EtOH) severely affects mitochondrial morphology in VL-17A cells.

A: After mitochondrial immunostaining using anti-Tom20 antibody, cells were classified according to their mitochondrial phenotype and examples of the three groups are shown. The distribution among the three categories was compared between untreated cells (ctrl) and cells exposed to 3 or 14 days of EtOH (D3, D14. 300 cells counted, $*P < 0.05$; scale bar= 10 μ m). **B:** Intracellular structure (**N**, nuclei) and megamitochondria (**M**) development were analyzed in untreated (ctrl) or in day3/day14 EtOH cultures. Representative electron micrographs show a mix of fragmented (circled areas) and elongated (squared areas) organelles in the ctrl and fragmented or megamitochondria (**M**; width, length >1 μ m; scale bar= 2 μ m) after EtOH exposure, especially at D14 of treatment. The graph shows the distribution of the size of megamitochondria in approx. 100 cells.

Figure 2. Ethanol (EtOH) exposure moderately reduces cell viability and severely affects cell growth, with no impact on mitochondrial respiration and mitochondrial mass in VL-17A hepatoma cell line. **A:** Cell growth rate decreases during culture in the presence of EtOH compared to the ctrl (mean \pm SEM; $n=4$, $*P < 0.05$). **B:** EtOH induces growth arrest as shown by changes in CellTrace dye fluorescence (mean \pm SEM; $n=4$). **C:** Apoptotic (Annexin-V(+)) and necrotic (Propidium Iodide(+)) cells (positive cells) were quantified after 3 days (D3, mean \pm SEM; $n=12$; $P > 0.05$) or 14 days (D14, mean \pm SEM; $n=7$; $*P < 0.05$) of EtOH exposure and compared to the untreated controls (ctrl). The longer treatment induces a small but significant increase in apoptosis. **D:** The mitochondrial functionality was investigated quantifying the oxygen consumption rate (OCR) in response to oligomycin, FCCP, or antimycin A and no significant differences are reported between the control and the EtOH-treated cells (mean \pm SEM; $n=3$, $P > 0.05$). **E:** The coupling efficiency and spare respiratory capacity were calculated and no significant difference is observed

between EtOH and ctrl (mean \pm SEM; $n=3$). **F:** The mitochondrial mass was analyzed after D3/D14 EtOH exposure with no differences detected (mean \pm SEM; $n=3$).

Figure 3. Ethanol (EtOH) exposure perturbs the Drp1 pathway in VL-17A cells. A:

Mitochondrial fragmentation: The expression or localization of Drp1 and its receptors (Mff, MiD51) were analyzed in the ethanol cultures after 3 or 14 days ($n>3$; D3, $P > 0.05$ and D14, $*P < 0.05$ compared to ctrl). **B:** Mitochondrial fusion: The expression of Mitofusin-1 (Mfn1) and Mitofusin-2 (Mfn2) was evaluated in untreated VL-17A cells (Ct) and after 3 or 14 days of EtOH exposure ($n>3$; D3, D14. $P > 0.05$). **C:** The hepatic expression of Drp1 was analyzed on WT mice fed with control or ethanol diet ($n=4$). In all panels representative western blots are shown along with the densitometric analysis (mean \pm SEM).

Figure 4. Drp1 inactivation promotes megamitochondria formation and reduces

ethanol-induced toxicity in hepatoma cells. A: Approx. 120 cells (positive for mtRFP and expressing Drp1-K38A (inactive form)) with/without 3days of EtOH exposure were sorted into three categories according to their mitochondrial morphology (hyper-fused/megamitochondria, mixed network, or hyper-fragmented) and a big proportion of cells with megamitochondria is detected ($*P < 0.05$). **B:** The three mitochondrial phenotypes were analyzed in VL-17A cells expressing WT Drp1 and positive for mtRFP (approx. 300 cells counted per condition). The distribution is different after 3 days of EtOH exposure (D3) compared to control ($*P < 0.05$). **C:** In VL-17A stably expressing eGFP (WT Drp1) or co-expressing eGFP and Drp1-K38A (Drp1-K38A) the number of GFP⁺ cells was quantified during 14 days of EtOH exposure. A significant increase is detected only in Drp1-K38A, but not in WT Drp1 (mean \pm SEM; $n=3$; $*P < 0.05$).

Figure 5. Ethanol exposure causes megamitochondria development in mice and hepatic Drp1 inactivation increases this effect and reduces ethanol-induced

hepatotoxicity. Megamitochondria formation was analyzed in mice with liver inactivation of Drp1 (Alb-Cre⁺Drp1) and compared to WT mice (Alb-Cre⁻Drp1) exposed to control or ethanol diet. **A, B:** Representative electron micrographs show examples of megamitochondria (**M**, megamitochondria: width, length >2 μ m; LD, lipid droplets; N, nucleus; scale bars= 1 μ m) in Alb-Cre⁻Drp1 (**A**) and Alb-Cre⁺Drp1 (**B**) fed with control or ethanol diet. **C:** The percentage of megamitochondria in Alb-Cre⁻Drp1 and Alb-Cre⁺Drp1 was quantified: a significant increase after ethanol exposure is seen in both groups and this effect significantly exacerbates after Drp1 inactivation (n>3; mean \pm SEM; >360 mitochondria analyzed; **P* < 0.05 vs Alb-Cre⁻Drp1 ctrl diet; †*P* < 0.05 vs Alb-Cre⁺Drp1 ethanol diet). **D:** ALT levels in the blood of Alb-Cre⁻Drp1 and Alb-Cre⁺Drp1 mice after exposure to ethanol were quantified and the ratios versus ALT in mice fed with control diet shown (ratio of mean \pm error propagation; n>3; **P* < 0.05).







